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<!--StartFragment-->RESULT 1
Q12621_HUMGT
ID   Q12621_HUMGT    PRELIMINARY;   PRT;   525 AA.
AC   Q12621;
DT   01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT   01-NOV-1996, sequence version 1.
DT   07-FEB-2006, entry version 31.
DE   Cellulase (EC 3.2.1.91).
GN   Name=cbh-1;
OS   Humicola grisea var. thermoidea.
OC   Eukaryota; Fungi; Ascomycota; mitosporic Ascomycota; Humicola.
OX   NCBI_TaxID=5528;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=IFO9854;
RA   Takashima S., Nakamura A., Hidaka M., Masaki H., Uozumi T.;
RT   "Cloning, sequencing, and expression of the cellulase genes of
RT   Humicola grisea var. thermoidea.";
RL   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: The biological conversion of cellulose to glucose
CC   generally requires three types of hydrolytic enzymes: (1)
CC   Endoglucanases which cut internal beta-1,4-glucosidic bonds; (2)
CC   Exocellobiohydrolases that cut the dissaccharide cellobiose from
CC   the nonreducing end of the cellulose polymer chain; (3) Beta-1,4-
CC   glucosidases which hydrolyze the cellobiose and other short cello-
CC   oligosaccharides to glucose (By similarity).
CC   -!- CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages
CC   in cellulose and cellotetraose, releasing cellobiose from the non-
CC   reducing ends of the chains.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; D63515; BAA09785.1; -; Genomic_DNA.
DR   HSSP; Q09431; 1GPI.
DR   GO; GO:0005576; C:extracellular region; IEA.
DR   GO; GO:0016162; F:cellulose 1,4-beta-cellobiosidase activity; IEA.
DR   GO; GO:0030248; F:cellulose binding; IEA.
DR   GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR   GO; GO:0030245; P:cellulose catabolism; IEA.
DR   GO; GO:0000272; P:polysaccharide catabolism; IEA.
DR   InterPro; IPR000254; CBD_fun.
DR   InterPro; IPR001722; Glyco_hydro_7.
DR   Pfam; PF00734; CBM_1; 1.
DR   Pfam; PF00840; Glyco_hydro_7; 1.
DR   PRINTS; PR00734; GLHYDRLASE7.
DR   ProDom; PD001821; CBD_fungal; 1.
DR   ProDom; PD186135; Glyco_hydro_7; 1.
DR   SMART; SM00236; fCBD; 1.
DR   PROSITE; PS00562; CBD_FUNGAL; 1.
KW   Carbohydrate metabolism; Cellulose degradation; Glycosidase;
KW   Hydrolase; Polysaccharide degradation.
SQ   SEQUENCE 525 AA; 55722 MW; A2E6E5F40F6D3BB0 CRC64;

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Query Match          99.8%;   Score 2799;   DB 2;   Length 525;
Best Local Similarity 99.8%;   Pred. No. 1.7e-184;
Matches 506; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 QQACSLTTERHPSLSWKKCTAGGQCQTVQASITLDSNWRWTHQVSGSTNCYTGNKWDTSI 60
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Db      19 QQACSLTTERHPSLSWKKCTAGGQCQTVQASITLDSNWRWTHQVSGSTNCYTGNKWDTSI 78

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↓ 10'

Qy	61	CTDAKSCAQNCCVDGADYTSTYGITTNGDSL	SLKFVTKGQHSTNVGSRTY	LM	DGEDKYQT	120
Db	79	CTDAKSCAQNCCVDGADYTSTYGITTNGDSL	SLKFVTKGQYSTNVGSRTY	LM	DGEDKYQT	138
Qy	121	FELLGNEFTFDVDVSNIGCGLNGALYFVSM	DADGGLSRYPGNKAGAKYGTGYCDAQCPRD	180		
Db	139	FELLGNEFTFDVDVSNIGCGLNGALYFVSM	DADGGLSRYPGNKAGAKYGTGYCDAQCPRD	198		
Qy	181	IKFINGEANIEGWTGSTNDPNAGAGRYGTCC	SEMDIWEANNMATAFTPHPCTIIGQSRCE	240		
Db	199	IKFINGEANIEGWTGSTNDPNAGAGRYGTCC	SEMDIWEANNMATAFTPHPCTIIGQSRCE	258		
Qy	241	GDSCGGTYSNERYAGVCDPDGCDFNSYRQGN	KTFYKGMTVDTTKKITVVTQFLKDANGD	300		
Db	259	GDSCGGTYSNERYAGVCDPDGCDFNSYRQGN	KTFYKGMTVDTTKKITVVTQFLKDANGD	318		
Qy	301	LGEIKRFYVQDGKIIIPNSESTIPGVEGNSIT	QDWCDRQKVAFGDIDDFNRKGGMKQMGKA	360		
Db	319	LGEIKRFYVQDGKIIIPNSESTIPGVEGNSIT	QDWCDRQKVAFGDIDDFNRKGGMKQMGKA	378		
Qy	361	LAGPMVLVMSIWDDHASNMLWLDSTFPVDAAG	KPGAERGACPTTSGVPAEVEAEAPNSNV	420		
Db	379	LAGPMVLVMSIWDDHASNMLWLDSTFPVDAAG	KPGAERGACPTTSGVPAEVEAEAPNSNV	438		
Qy	421	VFSNIRFGPIGSTVAGLPGAGNGGNNGGNPPP	TTTTSSAPATTTTASAGPKAGRWQQCG	480		
Db	439	VFSNIRFGPIGSTVAGLPGAGNGGNNGGNPPP	TTTTSSAPATTTTASAGPKAGRWQQCG	498		
Qy	481	GIGFTGPTQCEEPYTCTKLNDWYSQCL	507			
Db	499	GIGFTGPTQCEEPYTCTKLNDWYSQCL	525			

<!--EndFragment-->